

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2005, 12:06:06 ; Search time 20.4938 Seconds
(without alignments)
1674.182 Million cell updates/sec

Title: US-09-609-146-4

Perfect score: 2185

Sequence: 1 MSGMEKLNQASWIIQOKLED.....ALSSEQMSRTYQSFHNKT 415

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2185	100.0	415	2	US-09-875-076-12
2	2170	98.3	412	2	US-09-949-016-10101
3	2162	98.9	415	2	US-09-545-944-2
4	2162	98.9	415	2	US-10-215-619-2
5	2148	98.3	415	2	US-09-341-016A-1
6	1252	57.3	242	2	US-09-684-725-2
7	942	43.1	403	2	US-09-170-496D-114
8	942	43.1	403	2	US-09-170-496D-224
9	942	43.1	403	2	US-09-743-742B-4
10	942	43.1	403	2	US-09-743-742B-10
11	825.5	37.8	405	2	US-09-743-742B-2
12	825.5	37.8	405	2	US-09-743-742B-11
13	476	21.8	412	2	US-09-743-742B-8
14	471	21.6	418	2	US-09-743-742B-5
15	471	21.6	418	2	US-09-826-509-535
16	448	20.5	353	2	US-09-077-675A-3
17	448	20.5	353	2	US-09-077-675A-3
18	448	20.5	366	2	US-09-762-661A-7
19	448	20.5	366	2	US-09-743-475-6
20	447	20.5	366	2	US-09-170-496D-210
21	444	20.3	361	2	US-09-077-675A-8
22	444	20.3	361	2	US-09-077-674-8
23	444	20.3	366	2	US-09-077-675A-13
24	444	20.3	366	2	US-09-077-674-13
25	444	20.3	366	2	US-09-170-496D-88
26	444	20.3	366	2	US-09-743-742B-7
27	444	20.3	366	2	US-09-762-661A-5

28	444	20.3	366	2	US-09-364-425B-45
29	444	20.3	366	2	US-09-743-475-4
30	436.5	20.0	364	2	US-09-077-675A-16
31	436.5	20.0	364	2	US-09-077-674-16
32	436.5	20.0	364	2	US-09-762-661A-6
33	436.5	20.0	364	2	US-09-743-475-5
34	436.5	19.9	364	2	US-09-743-475-3
35	430	19.7	349	2	US-09-762-661A-2
36	417.5	19.1	353	1	US-08-118-270-45
37	417.5	19.1	353	4	PCT-US93-08528-45
38	410	18.8	415	2	US-09-743-742B-6
39	410	18.8	416	2	US-08-858-876A-4
40	410	18.8	416	2	US-09-472-880-4
41	405.5	18.6	398	1	US-08-288-663A-1
42	402	18.4	302	2	US-09-077-675A-2
43	402	18.4	302	2	US-09-077-674-2
44	398	18.2	302	4	US-09-077-675A-7
45	398	18.2	302	2	US-09-077-674-7

ALIGNMENTS

RESULT 1

US-09-875-076-12
; Sequence 12, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281

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OM protein - protein search, using sw model

Run on: November 19, 2005, 19:53:11 ; Search time 54.3086 Seconds
(without alignments)
3192.847 Million cell updates/sec

Title: US-09-609-146-4

Perfect score: 2185

Sequence: 1 MSGMEKLQNASWIYQOKLED.....ALSSQMSRTYQSPHFNKT 415

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2185	100.0	415	3	US-09-875-076-12
2	2185	100.0	415	3	US-09-876-252-12
3	2185	100.0	415	4	US-10-272-983-12
4	2185	100.0	415	4	US-10-393-807-12
5	2185	100.0	415	4	US-10-258-423-2
6	2185	100.0	415	4	US-10-417-820A-12
7	2185	100.0	415	4	US-10-723-955-12
8	2185	100.0	415	4	US-10-782-596-12
9	2185	100.0	415	4	US-10-203-015A-1
10	2185	100.0	415	4	US-10-770-583-2
11	2185	100.0	415	5	US-10-723-955-12
12	2185	100.0	415	5	US-10-745-237-396
13	2170	99.3	412	4	US-10-225-567A-557
14	2170	99.3	412	4	US-10-770-583-4
15	2166	99.1	415	4	US-10-203-015A-17
16	2162	98.9	415	4	US-10-770-583-6
17	2162	98.9	415	5	US-10-215-619-2
18	2148	98.3	415	5	US-10-890-407A-1
19	2147	98.3	412	4	US-10-770-583-8
20	2113	96.7	402	4	US-10-258-423-4
21	1650.5	75.5	395	4	US-10-258-423-6
22	1643.5	75.5	396	4	US-10-258-423-8
23	1409	64.5	296	4	US-10-203-015A-21
24	1394	63.8	293	4	US-10-770-583-10
25	1252	57.3	242	5	US-10-915-157-2
26	1251	57.3	249	3	US-09-782-974C-18
27					

28	1251	57.3	249	5	US-10-467-492A-18	Sequence 18, Appl
29	1251	57.3	249	5	US-10-975-979-18	Sequence 18, Appl
30	1251	57.3	249	5	US-10-969-727-18	Sequence 18, Appl
31	942	43.1	403	4	US-10-251-385-114	Sequence 114, Appl
32	942	43.1	403	4	US-10-251-385-224	Sequence 224, Appl
33	942	43.1	403	4	US-10-225-567A-540	Sequence 540, Appl
34	942	43.1	403	4	US-10-290-078-18	Sequence 18, Appl
35	942	43.1	403	4	US-10-353-690-10	Sequence 10, Appl
36	942	43.1	403	5	US-10-915-157-8	Sequence 8, Appl
37	941	43.1	426	4	US-10-712-124-116	Sequence 116, Appl
38	939	43.0	445	4	US-10-240-145-53	Sequence 53, Appl
39	939	43.0	445	4	US-10-240-145-139	Sequence 139, Appl
40	939	43.0	445	5	US-10-291-128-53	Sequence 53, Appl
41	939	43.0	445	5	US-10-291-128-139	Sequence 139, Appl
42	929	42.5	426	4	US-10-311-671-1	Sequence 1, Appl
43	929	42.5	426	6	US-11-100-583-1	Sequence 1, Appl
44	921	42.2	422	4	US-10-367-094-141	Sequence 141, Appl
45	804.5	36.8	403	4	US-10-367-094-138	Sequence 138, Appl

ALIGNMENTS

RESULT 1

US-09-875-076-12
; Sequence 12, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 60/157,280
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; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281

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OM protein - protein search, using sw model

Run on: November 19, 2005, 20:08:37 ; Search time 4.61111 Seconds
(without alignments)
101.661 Million cell updates/sec

Title: US-09-609-146-4
Perfect score: 2185
Sequence: 1 MSGEKLQNASWVQOKLED.....ALSSEQMSRTWYQSFHNKT 415

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	12.3	522	1	US-10-510-018-2
2	242.5	11.1	350	1	US-10-502-145-1
3	236.5	10.8	415	1	US-10-627-633-2
4	235	10.8	409	1	US-10-627-633-4
5	233	10.7	352	1	US-10-627-633-6
6	142.5	6.5	347	1	US-10-131-826A-18
7	85.5	3.9	446	7	US-11-082-389-316
8	81.5	3.7	693	1	US-10-131-826A-406
9	81	3.7	426	7	US-11-008-331-2
10	78.5	3.6	327	1	US-10-467-962B-107
11	77	3.5	472	7	US-11-008-331-3
12	75.5	3.5	765	1	US-10-131-826A-28
13	74	3.4	508	7	US-11-082-389-178
14	73	3.3	463	1	US-10-510-386-186
15	72.5	3.3	3056	7	US-11-109-156-20
16	70	3.2	628	7	US-11-082-389-402
17	69.5	3.2	263	7	US-11-082-389-120
18	69.5	3.2	278	7	US-11-082-389-118
19	69.5	3.2	453	7	US-11-082-389-198
20	69.5	3.2	926	1	US-10-841-129-2
21	69.5	3.2	928	1	US-10-841-129-6
22	68.5	3.1	464	1	US-10-689-742-164
23	68	3.1	435	1	US-10-510-386-62
24	68	3.1	928	1	US-10-841-129-4
25	67	3.1	348	7	US-11-082-389-218

26	67	3.1	582	7	US-11-074-176-110	Sequence 110, App
27	66	3.0	324	7	US-11-082-389-440	Sequence 440, App
28	66	3.0	480	7	US-11-074-176-2	Sequence 2, Appl
29	65.5	3.0	585	7	US-11-012-762-6	Sequence 6, Appl
30	65.5	3.0	1167	1	US-10-942-072-6	Sequence 6, Appl
31	65	3.0	394	7	US-11-074-176-310	Sequence 310, App
32	65	3.0	414	7	US-11-074-176-46	Sequence 46, Appl
33	65	3.0	643	7	US-11-074-176-318	Sequence 318, App
34	65	3.0	667	7	US-11-074-176-64	Sequence 64, Appl
35	64.5	3.0	135	7	US-11-082-389-414	Sequence 414, App
36	64.5	3.0	604	1	US-10-942-072-4	Sequence 4, Appl
37	64.5	3.0	1167	1	US-10-942-072-13	Sequence 13, Appl
38	64.5	3.0	1168	1	US-10-942-072-11	Sequence 11, Appl
39	64	2.9	849	1	US-10-467-962B-53	Sequence 53, Appl
40	63.5	2.9	391	7	US-11-082-389-172	Sequence 172, App
41	63.5	2.9	391	7	US-11-082-389-174	Sequence 174, App
42	63.5	2.9	395	7	US-11-074-176-188	Sequence 188, App
43	63.5	2.9	690	1	US-10-131-826A-306	Sequence 306, App
44	63.5	2.9	1049	1	US-10-131-826A-358	Sequence 358, App
45	63.5	2.9	2897	1	US-10-499-715-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-510-018-2
; Sequence 2, Application US/10510018
; Publication No. US20050244896A1

GENERAL INFORMATION:

; APPLICANT: Golz, Stefan
; APPLICANT: Weingarten, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TITLE OF INVENTION: Neuropeptide FF Receptor 2 (NPFF2)
; FILE REFERENCE: Le A 35 945
; CURRENT APPLICATION NUMBER: US/10/510,018
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/002962
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: EP 02007270.8
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-018-2

Query Match 12.3%; Score 268; DB 1; Length 522;
Best Local Similarity 22.3%; Pred. No. 6.4e-21;
Matches 90; Conservative 88; Mismatches 168; Indels 58; Gaps 13;

QY	25	HLNSTEYL-----AFLCGRSRSHFFLPVSVVYVIFVVGIVGNVLVLIOHQ 74
DB	120	NVNDTRHLYSDINITYVNYLHPQVAAIFI---ISYFLIFLCMGTWVCFVVRNK 176
QY	75	AMKTPNYLFSLVSDLLVLLGLMPLEVE-MWRNYPELPFGVGVCFKALFETVCFAS 133
DB	177	HHHTVNLNLALISDLVLGIPCMPTLLDNIAGWP--FGNTMKISGLVQGISVAAS 234
QY	134	ILSITTVSVERVAILHPFRALQSTRRALRILGLVWGFSLFSPNTSIHGKHYFP 193
DB	235	VTLVAIVDRQCVVYVPKPL--TIKTAFLIIMLIWLAITMSPVAMLVHVEEYK 292
QY	194	NSGLVPGSATCTV--IKPMW-----IYNFIQVTSFLF---YLLPMTVISVLYLMAL 241
DB	293	RVLANSQNTSPVYWCREDWPNQEMRKIV-----TTLFANIYLAFLSLIVIMYGRIGI 346
QY	242	RLKKDKSLSEADSGNAN-----IOPCKSVNKMFLVILVLPATCAWPHDRLFPSFVEW 297
DB	347	SLFRAAVPHTRGRKNOEQMHWVSRKKQKII-KMLLVALLFILSLWPLTMTMLSDYADLS 405

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OM protein - protein search, using sw model

Run on: November 19, 2005, 20:08:37 ; Search time 4.38889 Seconds
(without alignments)
101.681 Million cell updates/sec

Title: US-09-609-146-25

Perfect score: 2076

Sequence: 1 MGKLENASWTHDPLMKYLS.....GQSHHNTLWTAPCAGVP 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301	14.5	522	US-10-510-018-2	Sequence 2, Appli
2	252.5	12.2	409	US-10-627-633-4	Sequence 4, Appli
3	251.5	12.1	415	US-10-627-633-2	Sequence 2, Appli
4	247.5	11.9	352	US-10-627-633-6	Sequence 6, Appli
5	227.5	11.0	350	US-10-502-145-1	Sequence 1, Appli
6	147.5	7.1	347	US-10-131-826A-18	Sequence 18, Appli
7	95.5	4.6	582	US-11-074-176-110	Sequence 110, App
8	89	4.3	446	US-11-082-389-316	Sequence 316, App
9	77	3.7	453	US-11-082-389-198	Sequence 198, App
10	75	3.6	579	US-10-975-798-4	Sequence 4, Appli
11	75	3.6	580	US-10-975-798-3	Sequence 3, Appli
12	73.5	3.5	394	US-11-074-176-310	Sequence 310, App
13	73.5	3.5	414	US-11-074-176-46	Sequence 46, Appli
14	72.5	3.5	928	US-10-841-129-4	Sequence 4, Appli
15	71	3.4	928	US-10-841-129-6	Sequence 6, Appli
16	69.5	3.3	472	US-11-008-331-3	Sequence 3, Appli
17	69.5	3.3	508	US-11-082-389-178	Sequence 178, App
18	69	3.3	3056	US-11-109-156-20	Sequence 20, Appli
19	68.5	3.3	765	US-10-131-826A-28	Sequence 28, Appli
20	68.5	3.3	1049	US-10-131-826A-358	Sequence 358, App
21	67	3.2	628	US-11-082-389-402	Sequence 402, App
22	67	3.2	639	US-11-074-176-222	Sequence 222, App
23	66.5	3.2	1167	US-10-942-072-6	Sequence 6, Appli
24	66	3.2	693	US-10-131-826A-405	Sequence 406, App
25	65	3.2	926	US-10-841-129-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-510-018-2

; Sequence 2, Application US/10510018

; Publication No. US20050244896A1

; GENERAL INFORMATION:

; APPLICANT: Golz, Stefan

; APPLICANT: Bruggemeier, Ulf

; APPLICANT: Weingarten, Bernhard

; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with

; TITLE OF INVENTION: Neuropeptide F Receptor 2 (NPFF2)

; FILE REFERENCE: Le A 35 945

; CURRENT APPLICATION NUMBER: US/10/510.018

; PRIOR FILING DATE: 2004-10-01

; PRIOR APPLICATION NUMBER: PCT/BP2003/002962

; PRIOR FILING DATE: 2003-03-21

; PRIOR APPLICATION NUMBER: EP 02007270.8

; PRIOR FILING DATE: 2002-04-02

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2

; LENGTH: 522

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-510-018-2

Query Match 14.5%; Score 301; DB 1; Length 522;
Best Local Similarity 23.8%; Pred. No. 3.9e-23;
Matches 81; Conservative 83; Mismatches 151; Indels 26; Gaps 9;

QY 42 VAYALFLVGMGNLLVCMVIVRHQTLKPTNYLPSLAVSDLLVLLGLMPLIYE-MWH 100
DB 152 ISYFLFFLCMGNTVCCIVMKNKHTVNLFILNLAISDLLVGFCHPILLDNIIA 211
QY 101 NYPFLPGVGCYKPTALFETVCFASILSVTVSVRYVAIVHFPRAKLESTRRLRLS 160
DB 212 GMP--FGNTWCKISGLVQGISVAASVFTLVAIAVDRFCQVVPFKPKL--TKTAPVIIM 267
QY 161 LVWSRVSVPFLNNTSIGHIKFQHPNGSSVPGSATCTV--TKPMW-----VYNLIQA 211
DB 268 IIVLWLAITMSASVNLHVQEEKYKVRNLNSONKTSPTVWCREDWPNQEKRIYTVTLFA 327
QY 212 TSFLPYLPMTLISLVLYLMLGLLKE---DESLEANKVAVNIHRPSKSVTKLFLVLV 268
DB 328 N---LYLAPLSLIVIMYGRIGISLFPAAVPHTRGNKQEQHVVRKQKIKMLLIVALL 384
QY 269 FAICWTPHVDRLFRSFVEWETESLAAPVNLHVVSGVFYLSAVNPPIIYNLLSRFPRA 328
DB 385 FILSWLPLMTLMLSDYADLSPNELQINIYIYPPFAHMLAFGNSSVNPPIYGFNFENFR 444

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OM protein - protein search, using sw model

Run on: November 19, 2005, 19:53:11 ; Search time 51.6914 Seconds
(without alignments)
3192.847 Million cell updates/sec

Title: US-09-609-146-25

Perfect score: 2076

Sequence: 1 MGKLENASWIHDPLMKYLNS.....GOSSIHNTLTTAPCAGEVP 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pcp.*
- 3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pcp.*
- 4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pcp.*
- 5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2076	100.0	395	4	US-10-258-423-6
2	2076	100.0	396	4	US-10-258-423-8
3	2063	99.4	395	4	US-10-203-015A-21
4	1650.5	79.5	402	4	US-10-258-423-4
5	1650.5	79.5	412	4	US-10-225-567A-557
6	1650.5	79.5	412	4	US-10-770-583-4
7	1650.5	79.5	415	3	US-09-875-076-12
8	1650.5	79.5	415	3	US-09-876-252-12
9	1650.5	79.5	415	4	US-10-272-983-12
10	1650.5	79.5	415	4	US-10-393-807-12
11	1650.5	79.5	415	4	US-10-258-423-2
12	1650.5	79.5	415	4	US-10-417-820A-12
13	1650.5	79.5	415	4	US-10-723-955-12
14	1650.5	79.5	415	4	US-10-782-596-12
15	1650.5	79.5	415	4	US-10-203-015A-1
16	1650.5	79.5	415	4	US-10-770-583-2
17	1650.5	79.5	415	5	US-10-723-955-12
18	1650.5	79.5	415	5	US-10-745-237-396
19	1644.5	79.2	415	4	US-10-203-015A-17
20	1640.5	79.0	412	4	US-10-770-583-8
21	1640.5	79.0	415	4	US-10-770-583-6
22	1640.5	79.0	415	5	US-10-215-619-2
23	1632.5	78.6	415	5	US-10-890-407A-1
24	1117.5	53.8	293	4	US-10-770-583-12
25	1117.5	53.8	296	4	US-10-770-583-10
26	1035.5	49.8	242	5	US-10-915-157-2
27	1022.5	49.3	249	3	US-09-782-974C-18

ALIGNMENTS

RESULT 1

US-10-258-423-6

; Sequence 6, Application US/10258423

; Publication No. US20030211968A1

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: University of Virginia

; TITLE OF INVENTION: NEW NEUROMEDIN U RECEPTOR NMUR2/AND

; FILE REFERENCE: NUCLEOTIDES ENCODING IT

; FILE REFERENCE: 20658P

; CURRENT APPLICATION NUMBER: US/10/258,423

; PRIOR FILING DATE: 2002-10-24

; PRIOR APPLICATION NUMBER: 60/200,718

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 395

; TYPE: PRT

; ORGANISM: Rattus

US-10-258-423-6

Query Match 100.0%; Score 2076; DB 4; Length 395;

Best Local Similarity 100.0%; Pred. No. 4e-174;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKLENASWIHDPLMKYLNSIETLYLAHLCPKRSDDLSPVSVAYALIFLVGMGNLLVCM 60

Db 1 MGKLENASWIHDPLMKYLNSIETLYLAHLCPKRSDDLSPVSVAYALIFLVGMGNLLVCM 60

Qy 61 VIVRHQTLKPTNYLPLSLAVSDLLVLLGMPLEIYEMHNYPLFGVGCYKFTALFET 120

Db 61 VIVRHQTLKPTNYLPLSLAVSDLLVLLGMPLEIYEMHNYPLFGVGCYKFTALFET 120

Qy 121 VCFASILSVTTVSVERVAIVHPFRALRILSLVWSFVSFSLPNTSIHGK 180

Db 121 VCFASILSVTTVSVERVAIVHPFRALRILSLVWSFVSFSLPNTSIHGK 180

Qy 181 FOHPPNGSSVPGSATCTVTKPMVYNIIOATSFYILPMTLISVLYLMLGLRKDES 240

Db 181 FOHPPNGSSVPGSATCTVTKPMVYNIIOATSFYILPMTLISVLYLMLGLRKDES 240

Qy 241 LEANKVAVNIHRPSKSVTKMLFVLVFAICWTPPHVDLRFPSFVEEWTESLAAVNL 300

Db 241 LEANKVAVNIHRPSKSVTKMLFVLVFAICWTPPHVDLRFPSFVEEWTESLAAVNL 300

Qy 301 HVVSGVFFYLSSAVNPIIYNLSRRFRAFRNVVSTCKWCHPRHRPOGPPAKIIFLTE 360

Db 301 HVVSGVFFYLSSAVNPIIYNLSRRFRAFRNVVSTCKWCHPRHRPOGPPAKIIFLTE 360

Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 114, App
Sequence 540, App
Sequence 18, Appl
Sequence 10, Appl
Sequence 8, Appl
Sequence 116, App
Sequence 53, Appl
Sequence 139, App
Sequence 53, Appl
Sequence 139, App
Sequence 224, App
Sequence 224, App
Sequence 1, Appl
Sequence 1, Appl
Sequence 141, App
Sequence 138, App

28 1022.5 49.3 249 5 US-10-467-492A-18
29 1022.5 49.3 249 5 US-10-975-979-18
30 1022.5 49.3 249 5 US-10-969-727-18
31 952.5 45.9 403 4 US-10-251-385-114
32 952.5 45.9 403 4 US-10-225-567A-540
33 952.5 45.9 403 4 US-10-290-078-18
34 952.5 45.9 403 4 US-10-353-690-10
35 952.5 45.9 403 5 US-10-915-157-8
36 951.5 45.8 426 4 US-10-712-124-116
37 949.5 45.7 445 4 US-10-240-145-53
38 949.5 45.7 445 4 US-10-240-145-139
39 949.5 45.7 445 5 US-10-291-128-53
40 949.5 45.7 445 5 US-10-291-128-139
41 946.5 45.6 403 4 US-10-251-385-224
42 939.5 45.3 426 4 US-10-311-671-1
43 939.5 45.3 426 6 US-11-100-583-1
44 933 44.9 422 4 US-10-367-094-141
45 819 39.5 403 4 US-10-367-094-138

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OM protein - protein search, using sw model

Run on: November 19, 2005, 12:06:06 ; Search time 19.5062 Seconds
(without alignments)
1674.182 Million cell updates/sec

Title: US-09-609-146-25

Perfect score: 2076

Sequence: 1 MGKLENASWIHDFLMKYLS.....GQSSIHNTLTTAPCAGEVP 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/PTCUS COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1650.5	79.5	412	2	US-09-949-016-10101
2	1650.5	79.5	415	2	US-09-875-076-12
3	1640.5	79.0	415	2	US-09-545-944-2
4	1640.5	79.0	415	2	US-10-215-619-2
5	1632.5	78.6	415	2	US-09-341-016A-1
6	1033.5	49.8	242	2	US-09-684-725-2
7	952.5	45.9	403	2	US-09-170-496D-114
8	952.5	45.9	403	2	US-09-743-742B-4
9	952.5	45.9	403	2	US-09-743-742B-10
10	946.5	45.6	403	2	US-09-170-496D-224
11	840	40.5	405	2	US-09-743-742B-2
12	840	40.5	405	2	US-09-743-742B-11
13	499	24.0	418	2	US-09-743-742B-5
14	498	24.0	418	2	US-09-826-509-535
15	477.5	23.0	412	2	US-09-743-742B-8
16	465.5	22.4	364	2	US-09-743-742B-16
17	465.5	22.4	364	2	US-09-077-675A-16
18	465.5	22.4	364	2	US-09-077-674-16
19	465.5	22.4	364	2	US-09-762-661A-6
20	465	22.4	353	2	US-09-743-475-5
21	465	22.4	353	2	US-09-077-675A-3
22	465	22.4	364	2	US-09-077-674-3
23	465	22.4	366	2	US-09-743-475-3
24	465	22.4	366	2	US-09-762-661A-7
25	463.5	22.3	361	2	US-09-743-475-6
26	463.5	22.3	361	2	US-09-077-675A-8
27	463.5	22.3	366	2	US-09-077-674-8
28	463.5	22.3	366	2	US-09-077-675A-13

28 463.5 22.3 366 2 US-09-077-674-13 Sequence 13, Appl
29 463.5 22.3 366 2 US-09-170-496D-88 Sequence 88, Appl
30 463.5 22.3 366 2 US-09-743-742B-7 Sequence 7, Appl
31 463.5 22.3 366 2 US-09-762-661A-5 Sequence 5, Appl
32 463.5 22.3 366 2 US-09-364-425B-45 Sequence 45, Appl
33 463.5 22.3 366 2 US-09-743-475-4 Sequence 4, Appl
34 462.5 22.3 366 2 US-09-170-496D-210 Sequence 210, App
35 451 21.7 349 2 US-09-762-661A-2 Sequence 2, Appl
36 437 21.1 410 2 US-08-858-876A-2 Sequence 2, Appl
37 437 21.1 410 2 US-09-472-880-2 Sequence 2, Appl
38 436 21.0 410 2 US-09-826-509-537 Sequence 537, App
39 433.5 20.9 353 1 US-08-118-270-45 Sequence 45, Appl
40 433.5 20.9 353 4 PCT-US93-08528-45 Sequence 45, Appl
41 430.5 20.7 415 2 US-09-743-742B-6 Sequence 6, Appl
42 430.5 20.7 416 2 US-08-858-876A-4 Sequence 4, Appl
43 430.5 20.7 416 2 US-09-472-880-4 Sequence 2, Appl
44 427 20.6 410 2 US-09-200-090-2 Sequence 4, Appl
45 423 20.4 302 2 US-09-077-675A-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-10101
; Sequence 10101, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10101
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10101

Query Match 79.5%; Score 1650.5; DB 2; Length 412;
Best Local Similarity 79.4%; Pred. No. 6.1e-128;
Matches 312; Conservative 36; Mismatches 40; Indels 5; Gaps 1;
QY 1 MGKLENASWIH-----DPLMKYLSNTEBYLAHLGCPKRSDSLSPVSAVALIFLVGMGN 55
Db 1 MEKLNASWITQKLEDPFQKHLNSTEYLAFLCGPRSHFPFLPSVVVPIFVGVGN 60
QY 56 LLVCMVIVRHQTLKPTNYTLFSLAVSDLLVLLGMPLEIYEMWNYNPFPGVGCYFKT 115
Db 61 VLVLIVLILQHQAMKPTNYTLFSLAVSDLLVLLGMPLEIYEMWNYNPFPGVGCYFKT 120
QY 116 ALFETVCFASTLSVTTVSVERVVAIVHPRAKLSRTRRALRILSLVMSFSPVPSLPNTS 175
Db 121 ALFETVCFASTLSITTVSVERVVAIVHPRAKLSRTRRALRILSLVMSFSPVPSLPNTS 180
QY 176 IHGKIFQHFPGNSVPGSATCTVTKPMVYVNIITQATSFYLPMTLISLVLYLMGLRL 235
Db 181 IHGKIFHYFPGNSLVPGSATCTVIKPMWIYNIIFLIQVTSFLFYLLPMTVLSVLYLMGLRL 240
QY 236 KRDSLSLANKVAVNIHPRSRKSVTKMLFVLVLVPAICWTPPHVDRLPFPSVEEWTESLAA 295
Db 241 KKDKSLEADEGNANTIQPCRSVKNKMLFVLVLVPAICWAPPHIDRLPFPSVEEWSES LAA 300
QY 296 VFNLHVSVGVFFYLLSSAVNPILINLLSRRFRAFRNVVSPCTCKWCHPRHPQGPQAQKI 355